#3 ~~0280~~
~~o7~~ ω

OIPE

ENTERED
See p. 5

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/772,105

DATE: 02/09/2001
TIME: 11:06:59

Input Set : A:\SEQ LIST 0838.1001-009.txt
Output Set: N:\CRF3\02092001\I772105.raw

```
    3  <110> APPLICANT: Ozelius, Laurie J.
    4         Breakefield, Xandra O.
    6  <120> TITLE OF INVENTION: TORSIN, TORSIN-RELATED GENES, AND
    7         METHODS OF DETECTING NEURONAL DISEASES
    9  <130> FILE REFERENCE: 0838.1001009
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/772,105
C--> 12 <141> CURRENT FILING DATE: 2001-01-26
   14  <150> PRIOR APPLICATION NUMBER: US 09/218,363
   15  <151> PRIOR FILING DATE: 1998-12-22
   17  <150> PRIOR APPLICATION NUMBER: US 09/099,454
   18  <151> PRIOR FILING DATE: 1998-06-18
   20  <150> PRIOR APPLICATION NUMBER: US 60/050,244
   21  <151> PRIOR FILING DATE: 1997-06-19
   23  <160> NUMBER OF SEQ ID NOS: 90
   25  <170> SOFTWARE: FastSEQ for Windows Version 4.0
   27  <210> SEQ ID NO: 1
   28  <211> LENGTH: 2597
   29  <212> TYPE: DNA
   30  <213> ORGANISM: Homo sapien
   32  <220> FEATURE:
   33  <221> NAME/KEY: CDS
   34  <222> LOCATION: (568)...(1563)
   36  <221> NAME/KEY: misc_feature
   37  <222> LOCATION: (1)...(2597)
   38  <223> OTHER INFORMATION: n = A, T, C or G
   40  <400> SEQUENCE: 1
W--> 41 ctgaaaatag ctncttatta ttattattat tattattatt atttgcggga gggagcacag 60
W--> 42 tcttgctctg tctcccaggc tggagntgca gtggtgagat ctcggctcac tgcaatctcc 120
W--> 43 gcctcctggg ttcaagngca gttgctcatg tgtcagcctc cccagtagct agggctacag 180
   44 gtgcctacca ccacaccggc taattttata tttttagtag agacgtggtt tcaccatgtt 240
W--> 45 ggtcaggctg gtctcgaact cctgacctca ggtgatccgc ccncctcagc ctncccaaag 300
W--> 46 ggctgggatt acaggcagga gccaccatnc ctggnaaaaa taacgtccat aaacaaaaac 360
   47 acgtggccaa cagggcggag cagaaccgag tttccggaag caaaacaggg ctttgtaccg 420
   48 aacaaagatg gcggccgccg gcgtcgggag gagggctgcc ctgaagaaag atggcctccg 480
W--> 49 cgagaggagg aanccggaag cgtgggtctg gcggctgcac cggttcgcgg tcggcgcgag 540
   50 aacaagcagg gtggcgcggg tccgggcatg aag ctg ggc cgg gcc gtg ctg ggc 594
   51                                 Met Lys Leu Gly Arg Ala Val Leu Gly
   52                                  1               5
   54 ctg ctg ctg ctg gcg ccg tcc gtg gtg cag gcg gtg gag ccc atc agc  642
   55 Leu Leu Leu Leu Ala Pro Ser Val Val Gln Ala Val Glu Pro Ile Ser
   56  10              15                  20                  25
   58 ctg gga ctg gcc ctg gcc ggc gtc ctc acc ggc tac atc tac ccg cgt  690
   59 Leu Gly Leu Ala Leu Ala Gly Val Leu Thr Gly Tyr Ile Tyr Pro Arg
   60          30                  35                  40
   62 ctc tac tgc ctc ttc gcc gag tgc tgc ggg cag aag cgg agc ctt agc  738
   63 Leu Tyr Cys Leu Phe Ala Glu Cys Cys Gly Gln Lys Arg Ser Leu Ser
   64          45                  50                  55
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/772,105

DATE: 02/09/2001
TIME: 11:07:00

Input Set : A:\SEQ LIST 0838.1001-009.txt
Output Set: N:\CRF3\02092001\I772105.raw

```
66 cgg gag gca ctg cag aag gat ctg gac gac aac ctc ttt gga cag cat      786
67 Arg Glu Ala Leu Gln Lys Asp Leu Asp Asp Asn Leu Phe Gly Gln His
68         60                  65                  70
70 ctt gca aag aaa atc atc tta aat gcc gtg ttt ggt ttc ata aac aac      834
71 Leu Ala Lys Lys Ile Ile Leu Asn Ala Val Phe Gly Phe Ile Asn Asn
72     75                  80                  85
74 cca aag ccc aag aaa cct ctc acg ctc tcc ctg cac ggg tgg aca ggc      882
75 Pro Lys Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Thr Gly
76   90                  95                 100                 105
78 acc ggc aaa aat ttc gtc agc aag atc atc gca gag aat att tac gag      930
79 Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala Glu Asn Ile Tyr Glu
80             110                 115                 120
82 ggt ggt ctg aac agt gac tat gtc cac ctg ttt gtg gcc aca ttg cac      978
83 Gly Gly Leu Asn Ser Asp Tyr Val His Leu Phe Val Ala Thr Leu His
84             125                 130                 135
86 ttt cca cat gct tca aac atc acc ttg tac aag gat cag tta cag ttg     1026
87 Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys Asp Gln Leu Gln Leu
88         140                 145                 150
90 tgg att cga ggc aac gtg agt gcc tgt gcg agg tcc atc ttc ata ttt     1074
91 Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg Ser Ile Phe Ile Phe
92     155                 160                 165
94 gat gaa atg gat aag atg cat gca ggc ctc ata gat gcc atc aag cct     1122
95 Asp Glu Met Asp Lys Met His Ala Gly Leu Ile Asp Ala Ile Lys Pro
96 170                 175                 180                 185
98 ttc ctc gac tat tat gac ctg gtg gat ggg gtc tcc tac cag aaa gcc     1170
99 Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val Ser Tyr Gln Lys Ala
100                 190                 195                 200
102 atg ttc ata ttt ctc agc aat gct gga gca gaa agg atc aca gat gtg    1218
103 Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu Arg Ile Thr Asp Val
104                 205                 210                 215
106 gct ttg gat ttc tgg agg agt gga aag cag agg gaa gac atc aag ctc    1266
107 Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg Glu Asp Ile Lys Leu
108         220                 225                 230
110 aaa gac att gaa cac gcg ttg tct gtg tcg gtt ttc aat aac aag aac    1314
111 Lys Asp Ile Glu His Ala Leu Ser Val Ser Val Phe Asn Asn Lys Asn
112     235                 240                 245
113     agt ggc ttc tgg cac agc agc tta att gac cgg aac ctc att gat tat  1362
114 Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg Asn Leu Ile Asp Tyr
115 250                 255                 260                 265
117 ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac cta aaa atg tgt atc    1410
118 Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His Leu Lys Met Cys Ile
119                 270                 275                 280
121 cga gtg gaa atg cag tcc cga ggc tat gaa att gat gaa gac att gta    1458
122 Arg Val Glu Met Gln Ser Arg Gly Tyr Glu Ile Asp Glu Asp Ile Val
123                 285                 290                 295
125 agc aga gtg gct gag gag atg aca ttt ttc ccc aaa gag gag aga gtt    1506
126 Ser Arg Val Ala Glu Glu Met Thr Phe Phe Pro Lys Glu Glu Arg Val
127                 300                 305                 310
129 ttc tca gat aaa ggc tgc aaa acg gtg ttc acc aag tta gat tat tac    1554
```

```
130 Phe Ser Asp Lys Gly Cys Lys Thr Val Phe Thr Lys Leu Asp Tyr Tyr
131     315                 320             325
133 tac gat gat tgacagtcat gattggcagc cggagtcact gcctggagtt           1603
134 Tyr Asp Asp
135 330
137 ggaaaagaaa caacactcag tccttccaca cttccacccc cagctccttt ccctggaaga 1663
138 ggaatccagt gaatgttcct gtttgatgtg acaggaattc tccctggcat tgtttccacc 1723
139 ccctggtgcc tgcaggccac ccagggacca cgggcgagga cgtgaagcct cccgaacacg 1783
140 cacagaagga aggagccagc tccagccca ctcatcgcag ggctcatgat tttttacaaa 1843
141 ttatgtttta attccaagtg tttctgtttc aaggaaggat gaataagttt tattgaaaat 1903
142 gtggtaactt tatttaaaat gatttttaac attatgagag actgctcaga ttctaagttt 1963
143 ttggccttgt gtgtgtgttt tttttttaagt tctcatcatt attacataga ctgtgaagta 2023
144 tctttactgg aaatgagccc aagcacacat gcatggcatt tgttcctgaa caggagggca 2083
145 tccctgggga tgtggctgga gcatgagcca gctctgtccc aggatggtcc cagcggatgc 2143
146 tgccaggggc agtgaagtgt ttaggtgaag gacaagtagg taagaggacg ccttcaggca 2203
147 ccacagataa gcctgaaaca gcctctccaa gggttttcac cttagcaaca atgggagctg 2263
148 tgggagtgat tttggccaca ctgtcaacat ttgttagaac cagtcttttg aaagaaaagt 2323
149 atttccaact tgtcacttgc cagtcactcc gttttgcaaa aggtggccct tcactgtcca 2383
150 ttccaaatag cccacacgtg ctctctgctg gattctaaat tatgtgaatt ttgccatatt 2443
151 aaatcttcct catttatact attatttgtt acgttcaatc agaatccccg aaacctccta 2503
152 taaagcttag ctgccccttc tgaggatgct gagaacggtg tctttcttta taaatgcaaa 2563
153 tggctaccgt tttacaataa aattttgcat gtgc                             2597
```

```
155 <210> SEQ ID NO: 2
156 <211> LENGTH: 332
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapien
160 <400> SEQUENCE: 2
161 Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser
162  1               5                   10                  15
163 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
164             20                  25                  30
165 Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
166             35                  40                  45
167 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
168         50                  55                  60
169 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
170 65                  70                  75                  80
171 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
172                 85                  90                  95
173 Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
174                 100                 105                 110
175 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
176             115                 120                 125
177 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
178         130                 135                 140
179 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
180 145                 150                 155                 160
181 Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
182                 165                 170                 175
```

```
183  Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
184           180               185               190
185  Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
186           195               200               205
187  Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
188      210               215               220
189  Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
190  225               230               235               240
191  Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
192                   245               250               255
193  Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
194               260               265               270
195  Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
196           275               280               285
197  Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
198      290               295               300
199  Thr Phe Phe Pro Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
200  305               310               315               320
201  Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
202                   325               330
205  <210> SEQ ID NO: 3
206  <211> LENGTH: 3568
207  <212> TYPE: DNA
208  <213> ORGANISM: Homo sapien
210  <220> FEATURE:
211  <221> NAME/KEY: CDS
212  <222> LOCATION: (994)...(1863)
214  <221> NAME/KEY: misc_feature
215  <222> LOCATION: (1)...(3568)      /
216  <223> OTHER INFORMATION: n = A,T,C or G
218  <400> SEQUENCE: 3
219      tgatccgcct gcctcggcct cccaaagtgc tgggattaca ggcgtgagcg ccgcgcccgg 60
220      ccagcctgag acagtttcgc tcttgtcgcc caggctggag tgcagtggca cgatctcggc 120
221      taactgcaac ctccgcctcc tgggttcaag agattctcct gcctcaacct ccgagtagct 180
W--> 222  gggattacag gcgyscgccr csmcrsccag cntttttttt tttttttgag acagtttcgc 240
W--> 223  tcttgtcgcc aggctggagt gcagtgnnng anctcggcta actgcaactc cgcctcctgg 300
W--> 224  gttcaagaga ttctnctgcc tcaactcccg agtagctggg attataggng nccgcnacca 360
225      caccatctaa ttttttgtat ttttagtaga gacggggttt cgcacgttga gcaggctggt 420
226      ctcgaactcc tgacatcagg tgatccgccc gattcagctt cccaaagtgc tgggattaca 480
227      ggcgtgagca cggcgcccgg ccaaaaaaaa aatatttttt tttttttttt agatattttt 540
228      tcactcttgt tgcccaggct ggagtgaaat ggcgtgatct cggctcggcc tcccaaagtc 600
W--> 229  ctgggattac aggcgtgaca ccgngcccgg sccgaaaaaa twttttttaaa agaaaaaggg 660
230      aaacaaamag tctcctacac cttcgrccac tcccaagaac gatggsacss cctcctctyc 720
W--> 231  gnccctmacc aaccatggcc gncccnaagg gagtggggcg ggtctgcggg gcggaagtga 780
232      cgsacgagag gaagtccgtc ctgcgcttgg ccgcggggcg cctggctcag tggcttctgc 840
233      gggcttcgag gagcgggatg ttgcgggctg ggtggctccg ggcgcggcgg cgctggcgct 900
234      gctgctggcg gcccgagtgg tggcggagtt cgagcccatc accgtgggc tagccatcgg 960
235      gcaggtcggc catcaccggc tacctgtcct aca atg aca tct act gcc cgt tcg 1014
                                            Met Thr Ser Thr Ala Arg Ser
236
```

```
237                                    1                   5
239 ccg agt gct gcc ggc gag gag cgg ccg ctc aac gct tcg gct ctc aag   1062
240 Pro Ser Ala Ala Gly Glu Glu Arg Pro Leu Asn Ala Ser Ala Leu Lys
241         10                15                20
243 ctg gat ttg gag gag aag ctg ttt gga cag cat cta gcc acg gaa gtg   1110
244 Leu Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val
245     25                30                35
247 att ttc aag gcg ctg act ggc ttc agg aac aac aaa aat ccc aag aaa   1158
248 Ile Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys
249 40                45                50                55
251 cca ctg acc ctt tcc tta cac ggc tgg gct ggc aca ggc aag aat ttt   1206
252 Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe
253             60                65                70
255 gtc agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt   1254
256 Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser
257         75                80                85
259 aac ttt gtc cac ctg ttt gta tcg act ctg cac ttc cct cat gag cag   1302
260 Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln
261         90                95                100
263 aag ata aaa ctg tac cag gac cag tta cag aag tgg atc cgc ggt aat   1350
264 Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn
265     105                110               115
267 gtg agt gca tgt gcg aac tct gtt ttc ata ttt gac gag atg gat aaa   1398
268 Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys
269 120               125               130               135
271 ttg cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac   1446
272 Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr
273             140               145               150
275 gag cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc   1494
276 Glu Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu
277         155               160               165
279 agc aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg   1542
280 Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp
281         170               175               180
283 cgg gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct   1590
284 Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro
285     185               190               195
287 gta ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac   1638
288 Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His
289 200               205               210               215
291 agt gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg   1686
292 Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu
293             220               225               230
295 cct ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg   1734
296 Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg
297         235               240               245
299 gcc cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag   1782
300 Ala Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu
301     250                 255               260
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/772,105

DATE: 02/09/2001
TIME: 11:07:01

Input Set : **A:\SEQ LIST 0838.1001-009.txt**
Output Set: **N:\CRF3\02092001\I772105.raw**

```
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:907 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1056 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:1604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:1621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:1735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:1736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:1751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/772,105

DATE: 02/09/2001
TIME: 11:07:01

Input Set : A:\SEQ LIST 0838.1001-009.txt
Output Set: N:\CRF3\02092001\I772105.raw

L:1775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:1827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88